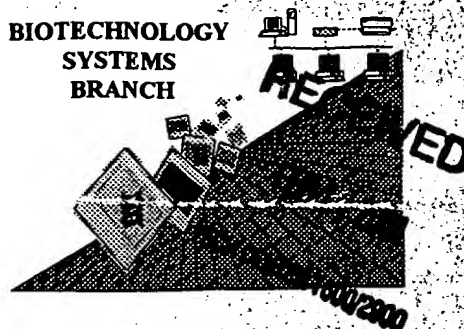


906

RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/375,924B

Source: 1644

Date Processed by STIC: 2/5/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/375,924B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
 Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1644

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/375,924B

DATE: 02/05/2001
 TIME: 14:51:42

Input Set : A:\abgx-2 cip.ST25.txt
 Output Set: N:\CRF3\02052001\I375924B.raw

p. 2
**Does Not Comply
 Corrected Diskette Needed**

3 <110> APPLICANT: Gallo, Michael
 4 Poord, Orit
 5 Junghans, Richard
 7 <120> TITLE OF INVENTION: GENERATION OF MODIFIED MOLECULES WITH INCREASED SERUM HALF-LIVES
 9 <130> FILE REFERENCE: ABGX-2 CIP
 11 <140> CURRENT APPLICATION NUMBER: US 09/375,924B
 12 <141> CURRENT FILING DATE: 1999-08-17
 14 <150> PRIOR APPLICATION NUMBER: US 60/096,868
 15 <151> PRIOR FILING DATE: 1998-08-17
 17 <160> NUMBER OF SEQ ID NOS: 10
 19 <170> SOFTWARE: PatentIn version 3.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 16
 23 <212> TYPE: PRT
 24 <213> ORGANISM: homo sapiens
 26 <400> SEQUENCE: 1
 28 Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr His Thr Cys Pro Pro
 29 1 5 10 15
 31 <210> SEQ ID NO: 2
 32 <211> LENGTH: 16
 33 <212> TYPE: PRT
 34 <213> ORGANISM: Artificial Sequence
 36 <220> FEATURE:
 37 <221> NAME/KEY: misc_feature
 38 <222> LOCATION: ()..()
 39 <223> OTHER INFORMATION: modified from human IgG1 hinge region
 42 <400> SEQUENCE: 2
 44 Ala Glu Pro Lys Ser Ser Asp Lys Thr His Thr His Thr Cys Pro Pro
 45 1 5 10 15
 47 <210> SEQ ID NO: 3
 48 <211> LENGTH: 12
 49 <212> TYPE: PRT
 50 <213> ORGANISM: Homo sapiens
 52 <400> SEQUENCE: 3
 54 Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro
 55 1 5 10
 57 <210> SEQ ID NO: 4
 58 <211> LENGTH: 12
 59 <212> TYPE: PRT
 60 <213> ORGANISM: Homo sapiens
 62 <400> SEQUENCE: 4
 64 Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro
 65 1 5 10
 67 <210> SEQ ID NO: 5
 68 <211> LENGTH: 12
 69 <212> TYPE: DNA
 70 <213> ORGANISM: Homo sapiens

*many of the same
 errors as previous
 submission*

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/375,924B

DATE: 02/05/2001
 TIME: 14:51:42

Input Set : A:\abgx-2 cip.ST25.txt
 Output Set: N:\CRF3\02052001\I375924B.raw

72 <400> SEQUENCE: 5
 73 tctctgggta aa
 76 <210> SEQ ID NO: 6
 77 <211> LENGTH: 12
 78 <212> TYPE: DNA
 79 <213> ORGANISM: Artificial/Unknown
 81 <220> FEATURE:
 82 <221> NAME/KEY: misc_feature
 83 <222> LOCATION: ()..()
 84 <223> OTHER INFORMATION: modified sequence
 87 <400> SEQUENCE: 6
 88 tccttaggga ag
 91 <210> SEQ ID NO: 7
 92 <211> LENGTH: 22
 93 <212> TYPE: DNA
 94 <213> ORGANISM: Artificial/Unknown
 96 <220> FEATURE:
 97 <221> NAME/KEY: misc_feature
 98 <222> LOCATION: ()..()
 99 <223> OTHER INFORMATION: primer 1
 102 <400> SEQUENCE: 7
 103 gggacccacg ggtgcgagg gc
 106 <210> SEQ ID NO: 8
 107 <211> LENGTH: 36
 108 <212> TYPE: DNA
 109 <213> ORGANISM: Artificial/Unknown
 111 <220> FEATURE:
 112 <221> NAME/KEY: misc_feature
 113 <222> LOCATION: ()..()
 114 <223> OTHER INFORMATION: primer 2
 117 <400> SEQUENCE: 8
 118 cttccctaag gacatggaga ggcctctctg tgtgtg
 121 <210> SEQ ID NO: 9
 122 <211> LENGTH: 36
 123 <212> TYPE: DNA
 124 <213> ORGANISM: Artificial/Unknown
 126 <220> FEATURE:
 127 <221> NAME/KEY: misc_feature
 128 <222> LOCATION: ()..()
 129 <223> OTHER INFORMATION: primer 3
 132 <400> SEQUENCE: 9
 133 gattccttag ggaaggcaga gcccaaatct agtgac
 136 <210> SEQ ID NO: 10
 137 <211> LENGTH: 34
 138 <212> TYPE: DNA
 139 <213> ORGANISM: Artificial/Unknown
 141 <220> FEATURE:
 142 <221> NAME/KEY: misc_feature
 143 <222> LOCATION: ()..()

12

12

22

36

36

invalid response - per 1.823 of new Sequence Rules, the only valid <213> responses are: Unknown or Artificial Sequence or Scientific name (Genus/species)

one of the three

(see circled portion of item 12 on Env Summary sheet)

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/375,924B

DATE: 02/05/2001

TIME: 14:51:42

Input Set : A:\abgx-2 cip.ST25.txt
Output Set: N:\CRF3\02052001\I375924B.raw

144 <223> OTHER INFORMATION: primer 4
147 <400> SEQUENCE: 10
148 gccggaattc ggtacgtgcc aagcatcctc gtgc

34

VERIFICATION SUMMARY

DATE: 02/05/2001

PATENT APPLICATION: US/09/375,924B

TIME: 14:51:43

Input Set : A:\abgx-2 cip.ST25.txt

Output Set: N:\CRF3\02052001\I375924B.raw